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PCT/NZ99/00107

SEQ ID NO: 1

GAATTCTTCTATGGCTATCACCATGTCCA	-10374
AAACACTACCTGAGTAAAGAAGGAGTCATTTTTTTTTTAAGGCTTTAAAA	-10324
AATTTAAAAATTTTAAATTAAATTTAAAAATGAAATCTAAAAAAATTTT	-10274
AAGAAAAATTTTTTTTAATCTGCAGAAACATACTCTGTATTGAGTCTATG	-10224
GTTACCAAAGATCCCCCAGAACAAAACCCCAAGAATTGCAAGATTTTCT	-10174
CTTGGAAGTGTTTGTCTTACTGGAAGGCTTATTAAGTCAATAATAAGGGA	-10124
GAGTAAAGACTTCAAACTAAAGATCTGTTTTTGTGAGTTCAATCTATAT	-10074
TGTCATCTGCTCTGGAAACCCTGAGCTTGTTCTAAAGTAACTGAACTAT	-10024
CATGAAGAAAATCAGCCATCAAAATAGTGAAAACGAACCTCTTACACTCA	-9974
GTTTTTTCTCATTTGTAAATTTAAAAAATTTAACTTCATTAAGTCTGGGG	-9924
ACCAATGTATAGCTGCAAGCAGGAATTTTATGCCTTCTTAATCCAGAGAG	-9874
GTGGGCAATGGTGTGGGTTTAGACCAGAAGTAAGGATGTGGGTGCAGCAA	-9824
ATATGACAGCCCAACTGCTGCTGCTGCTGCTAAGTCACTTCAGTCGTGTC	-9774
CGACTCTGTGTGACCCAGAGACGGCAGCCACCAGGCTCCCCCGTCCCT	-9724
GGGATTCTCCAGGCAAGAACAACACTGGAGTGGGTTGCCATTTCTCTCCAA	-9674
TGCATGAAAGTGAAAAGTGAAAGTGAAGTCGCTCAGTCGTGTCGACCCCT	-9624
CAGTGACCCCATGGACTGCAGCCTACCAGGCTTCTCCGTCCATGGGATTT	-9574
TCCAGGCAAGAGTACTGGAGTGGGGTGCCATTGCCTTCTCCATGACAGCC	-9524
CAACTAGAGACTGCTATAACTTATATCAGAGAATCTGAAACTCCCTACAG	-9474
GCTATCTTGCTATATGTGCATTCAACATGAACAAAAAGAAAATTCAAGTC	-9424
CAGTAAAAAGGGCTAAAATAGTGAATCACAGACTTTTGCCAAACAACAGT	-9374
CAATGATTTGGGCAAAGGACTTAAGTAGCTATGCTTATTTGCTATTAGTA	-9324
GAATAAAGAAATGTTTGAGCCTGGTTCTCAATGCTTGAATAATAAGATTC	-9274
CTTTTCAAGGAAAAACAATTTTTTTGAGAACTCATAGATAAAAGTCAAAT	-9224
CTATCACTTTAGATGTCACTTGAAGCCAACTTGATTATAGTAAACAAATT	-9174
CAGCTGTAAACATTTTTTTTATAACACTGTAGACACTGTATTTTTATACAC	-9124
TGTATAAATGAAGACACTGAAGATGTAAAGTGGTGACCTGGATGATCCAG	-9074

Fig 1

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AATATGCAATATGCACCAAAACTAAGTTTTTTAAATGATACAAATGAAC	-9024
TTACTTACAAAAGGGAAATAGAGTCACAGATGTAGAAAACATACAGTTAC	-8974
CTAGGGGGACGGGGGGAGGGTAAACTGGGAGATAGGAATTGACACATACA	-8924
CTCTACTATATATACACTAGGTAACATAATGAACCTACTGTATAGCGCA	-8874
CAGAACTCTACCCAATACTCTGTAATGACATTTATGGGAATAGAATCCAA	-8824
AAAGAGCAGATATGTGTATATGTATAAACTGATTCACACCCCTTGCCTTG	-8774
CCTAAACACACACAGACACACACAGACACATCCATTTTGAGATTTCTTTC	-8724
CTCCTCTTTGGCTACTTTTGACTCAGTTTGACCTAGATAGGACCTGTGCT	-8674
GGGTAAGGGCTTTGGCAGTCTTAAGTAGTGTGAGAGCAAGCACAGTCACT	-8624
CCCTAGCAAGGTCTTATTACTAGCTACAGAGTCTCTCTGTGCAGTCATAG	-8574
ATCACTGAGTGCAAAAGTCCAGTGCAATGTTTGAGTCCCATGCATGCTCT	-8524
CACAGAACTGAGAGAGGAGGCAAGGACACAGGACCCTCCAGTGCTGGGAC	-8474
TCTCTACTGGGGTGAGCAAGAGGGAACCCAATAGAAATGCTGCGAACCAC	-8424
AGAGCCACTCAGAAAGCCTGTAAATATAAACATAACAACACATTATGAAT	-8374
ATATAAGTATAAGTATACCTACCAAAAAATCAGAAAGTTGAACTTTTTTG	-8324
TATTCAAGGGAACAGTCATTCATTTATCGGTTTCAGTTATCAGTAAACACA	-8274
TTTGGGAACTGTAAAAATCTAATCAGTTCAGTTCAGTTCAGTCGCTCAGT	-8224
CGTGTCTCTTTGCGACTCCATGAATCGCAGCACGCCAGGCCTCCCTGTCT	-8174
ATCACCAACTCCCGGCGTTCACTCAGACTTACGTCCATCGAGTCAGTGAT	-8124
GCCATCCAGCCATCTCATCCTCTGTCTGTCCTCCCTTCTCCTCCTGCCCCAA	-8074
TCCCTCCCAGCATCAGAGTCTTTTCCAATGAGTCAACTCTTCTCACGAGG	-8024
TGGCCAAAGTACCAAGTCTTTGAGTCTAGTCTCTTTTTTCAATGGAGAAG	-7974
AAGAGGAAACCAAATTATAACTTAATTTTTATTCTTTGTATTACAAGTGT	-7924
ATAATTAATACACTGGAGTTTCCATTTTCAGAAAGGAAGAAGAGAAATCAC	-7874
ATTTTGCAGCTTTCCTGAACTAATACAAAGAAATGCAGAAGTTTGTAA	-7824
CTGGGATATTATTATGACACGTTGCCATAATATGAATGTCATCATCTCAA	-7774
GACTGACCTGAAAACCAAAATAAAAAAAAAAAGAGAGAGAGAGAGAGA	-7724

Fig 1 contd

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GAGAGAAAAAAAGAAAACCCTCCAGACCAGATTTTCAGTCTACCACTTGA -7674  
GCTGACAAACATTGGCCAAATGTCCTCTACAGAACCTGTAAGTTAGTAGT -7624  
TGGTAATTATAAAACAATAAAGTATATATTTCTGCTCCTGGCAATAATTA -7574  
TGTATCAGTTAAAAAGTATACATTGTCTAAAAAATCACCATATTTGATGT -7524  
CTCATTAAAACAAAGTTACAAATATTAAGATGAGAGGACTTAAAGTTAGA -7474  
TGGGAAAATATTCAATTGAAGCAGTATAAAATGCATTACTCTGGGGCAAA -7424  
GTGTGGTCTGGAGATCCCTGGAGTGAAGACCCTTTTAGACAATCTGTGGA -7374  
GTAAGAACTGTTTTTCATAACAAAGCTAAGATTTCCCTTGCTATTCTCATTT -7324  
TCTCTTACGTATATAGTCGAGTTTTCCAGAAGTTCCATGTTATGTAACAT -7274  
CATCATTA CTCTGTCAGCAAATAGAATACATGTTTGCATATGTCTATATT -7224  
CTAACATTTCTCATTTTTTAATTTATAATTCATTAAATATTGATAGATATG -7174  
ACCCACATAAAACAAAAGCTTTTCAGGATCCTGAATAACTTTTCAGAGTAA -7124  
AGGAATCTTGAGACCAAAGGTTTGAGAATTACTGTTTTAGGGGATACAC -7074  
CTCAAGTGAAAGAGCACGCCTCATCACATTTCCACTCTATATGGAAGAAT -7024  
CTAGAAGATTGAACCTATAATTGAAGAGTGCAGGCTTTATGAAGACAGTG -6974  
ACTGTTTCTGTCTGCTTTCTCCTCAGAATTTAGCATGATGCCAGGCACAT -6924  
AATTTGTTGTTGTTTCAGCTGCTAAGTCATCTCTGACTTTTTTGCAACCCCA -6874  
TGAAGTGCATGCAACATGCCAGGTTTCTCTGCTTTCACTATCTCCTGGAG -6824  
TTTGCTCCAACTCATGTCCATTGAGTCACTGATACCATCCAACGATCTCA -6774  
TCCTCTATAAGACACATTATAGACATTAGAATATTTTCATAAAATAATAA -6724  
GTGAATTAATACAGCTGAAACTCAAACAGCATAGGGGTTACAAGTACCAA -6674  
CTCGCGTCCAAGTTGAAAATCCACATATAATCTTAAGGTCAGCCTTGAT -6624  
ACATGCATATCCAAGGTTCCCCATCTGAGGATTCAACCAACCTCAGATAG -6574  
TGTAAGTACTGCAGTACACATTTAGTGAAAAATGTGCATATAAGTGGACCC -6524  
ATGCAGGTCAAACCTGCGTTTTTCCAAGGGTCCACAGTACACACACACATG -6474  
CATACATGCATCTCTAAATGAAAGCTTTGCCATCTGACTTACTCAAGGTC -6424  
ACATAAAACGTCAGCGAGAAACCCAGAACTATATTCAGATCTCTGTTCC -6374

Fig 1 contd

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TATACTGTTACTCCCTGAGTCAAGGGTACTTTTGTGTTTGTTCATTTTTTA	-6324
TTCTGTAATCTATTGAGATCACAGATAATCAGATGTTGCCACTGTAGGAT	-6274
GGCAGCCTCTCATGCTGTTATGTGAATTGAGCACTATCCAGTTTGTGTTCT	-6224
GGCTTTAAGTGTAATCAGAACAGTGTTATATCAAAGGGCTATCATCACAA	-6174
GGAAATGGCAAGAGTGATCAGATAAAATGCATCTTTCTCTCTTTTCCCAC	-6124
AACAGACTCGAATTTTTTCATGATTCAATCCTTATTCTAATTCTTCAGTTCA	-6074
GTTTCAGTTTCAGTCCTTCAGTCATGTCCAACCTTTTGCCACCCCATGAATC	-6024
TCAGCAAGCCAGGCCTCCCTGGTCCATCACCAACTCCCAGAGTTCACCCA	-5974
GACTCACGTCCATCGAGTCAGTGATGCCATCTAGCCATCTCATCCTCTGT	-5924
CGTCCCCTTCTCTTCCTGCCCCCAATCCCTCCCAGCATCAGAGTCTTTTC	-5874
CAATGAGTCAACTTTTCACATGAGGTGGCCAAAGTACTGGAGTTTCAGCT	-5824
TTAGCATCATTCCTTCCAAAGAAATCCCAGGGCTGATCTCCTTCAGAATG	-5774
GACTGGTTGGATCTCCTTGCAGTCCAAGGGACTCTCAAGAGTCTTCTCCA	-5724
ACACCACAGTTCAAAAGCATCAATTCTTCGGCGCTCAGCTTTCTTCACAG	-5674
TCCAACTCTCACATCCATACATGACCACAGGAAAAACCATAGCCTTGACT	-5624
AGATGGACCTTTGTTGGCAAAGTAATGTCTCTGCTTTTCAATATGCTATC	-5574
TAGGTTGGTCATAACTTTCTTCCAAAGGAGTAAGCATCTTTTAATTTTCAT	-5524
GGCTGCAGTCACCATTTGTAGTGATTTTGGAGCCCAGAAAAATAAAGTCT	-5474
TGACACTGTTTCCACTGTTTCCCCATCTTATTTCCCATGCAGTGATGGGA	-5424
CCGGATGCCATGATCTTAGTTTTCTGAATGTTGAGCTTTAAGCCAACTTT	-5374
TTCAATCTCCTCTTTCACTTTCATCAAGAGGCTTTTGAGTTCCTCTTCAC	-5324
TTTCTGCCATAAGGGTGGTGTCATCTGCATATCTGAGGTTATTAATATTT	-5274
CTCCCGGCAATCTTGATTCCAGCTTGTGCTTCTTCCAGCCCAGTGTGTTCT	-5224
CATGATGTACTCTGCATAGAAGTTAAATAAGCAGGGTGACAATATACAGT	-5174
CTTGACATCCTCCTTTTCCTATTTGGAACCAGTCTGTTGTTCCATGTCCA	-5124
GTTCTAACTGTTGCTTCCTGACCTGCATACAGGTTTCTCAAGAGGCAGGT	-5074
CAGGTGGCAGGTCAGGTGGTCAGGAACATCTCTTTCAGAATTTTGGACAG	-5024

Fig 1 contd

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TTTATTGTGATCCACACAGTCAAAGGCTTTGGCATAGTCAATAAAGCAGA	-4974
AATAGATGTTTTTCTGGAACCTCTCTTGCTTTTTTCGATGATCCAGCAGATG	-4924
TTGGCAATTGATCTCTGGTTCCTCTGCCTTTTCTAAAACCAGCTTGAAC	-4874
ATCAGGAAGTTCATGGTTCACGTATTGCTGAAGCCTGGCTTGGAGAATTT	-4824
AGAGCATTACTTTACTAGCATTACTTTTCACAATAAACTGTGGAAAATTC	-4774
TGAAAGAGATGGGCATACCAGACCACCGGATCTGCCTCTTGAGAAATTTG	-4724
CATGCAGGTCAGGAAGCAACAATTAGAAGTGGACATGGAACAACAGACTG	-4674
GTTCCAAATAGGAAAAGGTGTTTCGTCAAGGCTGTATATTGTCACCCTGTT	-4624
TATTTAACTTCTATGCAGAGTACATCATGAGAAACGCTGGGCTGGAAGAA	-4574
GCACAAGCTGGAATCAAGATTTCCGGGAGAAATATCAATAACCTCAGATA	-4524
TGCAGATGACACCACCCTTATGGCAGAAAGTGCAGAGGAACTAAAAAGCC	-4474
CCTTGATGAAAGTGAAAGTGGAGAGTGAAAAAGTTGGCTTAAATCTCAAC	-4424
ATTCAGAAAACGAAGATCATGGCATCCGGTCCCATCACTTCATGGGAAAT	-4374
AGATGGGGAAACAGTGGAACAGTGTGAGACTTTATTTTTCTGGGCTCCA	-4324
AAATCACTACAAATGGTGACTGCAGCCATGAAATTAAAAGATGCTTACTC	-4274
CTTGGAAGGAAAGTTATGACCAACCTAGATAGCATATTGAAAAGCAGAGA	-4224
CATTACTTTGCTAACAAAGGTCCATCTAGTCAAGGCTATGGTTTTTCCTG	-4174
TGGTCATGTATGGATGTGAGAGTTGGACTGTGAAGAAAGCTGAGTGCCGA	-4124
AGAATTGATGCTTTTGAACTGTGGTGTGAGAGAAGACTCTTGAGAGTCCC	-4074
TTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTG	-4024
GGATTTCTTTGGAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGC	-3974
CACCTCATGTGAAGAGCTGACTCATTGGAAAAGACTCTGATGCTGGGAGG	-3924
GATTGGGGGCAGGAGGAGAAGGGGGCGACAGAGGATGAGATGGCTGGATG	-3874
GCATCACTGACTCAATGGACGTGAGTCTGTGTGAACTCTGGGAGTTGGTG	-3824
ATGGACAGGGAGGCCTGGCGTGCTTTGATTCATGGGGTCACAAAGAGTCG	-3774
GACACGACTGAGCGACTGATCTGTCTCTCTTACTAGCATGTGTCTCCT	-3724
CCTTTTTTTGCCACATCATCAAACCTCCTGGCAAACCTCACATTAATAACA	-3674

Fig 1 contd

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TTTGGGAGCTTCCAGAATGCAAACAGTGAAACCATTAATGTTTTTTGGGA	-3624
AATATGCTTTTATACTCTCAATGTTGTTTTGAAACGCACACCCCCCTCCCCT	-3574
GCCGCCTGGTGTGTTGTAAGACAGTTGAGAGAAGTTTGCTTGCTACCTTAC	-3524
TTATGGTTACACAAACGTAAGGCCCCCTGAGTACAAAGAAGAACAGGGGG	-3474
AACGCAAACCTTCAGGCCCTGTGAGGAGGGGCACTGGACTCCTGTGAGAAG	-3424
AAACTGCTTTCAAAGAATTCCTGGGAGAAATTCTCTATGCACTCATCCTA	-3374
GCAACAAAGTCCTGTCCGAAGTTAGGCCCGCAGCACCCACACGGCAGTGA	-3324
AGGTTCCCTACTGCTGGTGAACCTTGCTGCTCCGAAGCCATAGGAAGGTTG	-3274
CAAATCCCGGCACTGGAGAAGGAAAACACGTTCTTGAAATTTCTTGAGTA	-3224
CCTCTTAATTCATTCAATGCTGACCTCCGGAGATTGGATAGAGCTGACTC	-3174
TCATTATTACAGTGGTTATGTTCTACCCAATCACTGCCAACATGAATAA	-3124
GTGATTCCCTGAACCACTGCCCCCTAGGGGAACTACAAGGTTAGATTCCCGT	-3074
CAGCCTCTGGTCACGTTTTTTGTTAACCAATCAATAAAATAACCTTGTTTTG	-3024
TGTGCATTTCTGTTTTTAAAATATCTTTATTTAATACGTACTGCTAATTCT	-2974
TCAACATTTGGTTCACAACCAAAAAGGCCCTATTAAGTGAAGCCCTGAAT	-2924
GAAGCTTACATAACACACATTGTTTTTCTATGAGGAAAAATTTTTTCCTTC	-2874
AGTCCTGCCACAGCCTTCTTGCTTAAAATTGTGGACAAAATATACATAAC	-2824
ATGAAACTGACTATTATTTAACTGATTTTAACTGTACAGTTCAGTGGCAT	-2774
TAAGTACACTTACCTTGCTGTGGAACCTATGATCAACATTCATCTCTAGAA	-2724
CTTTTTGATCTTCTCGAATTGAAAACCTCTGCATCTATTGCACAGTAGCTT	-2674
TCCCCCATCACACCGCACCCCTTCCTCCAGCCCCCGGCACCACCATCCTT	-2624
CTTTCCATGACAGTCATCCTGTGCCTAGGAACACAGCCCTTCAACACTAC	-2574
GCTTGGGGGGCACTGTAAGCAACAGGATCACTCCCTACCGCCACCAAATG	-2524
CACACAAAAATATAAAAAGCATGGTGGCATATCGATTGCAAAAAGGGTGC	-2474
TTGCTAAGTATGAGGGCTGAAACAAGGCAGAGAATTGACTAGGTTGACCT	-2424
CAGCTGGGATCCTGTGTGTTGGAAGCCTCAAATTTTCCATTGTTCTGTGC	-2374
ATACGCACAAATGCTTATAAAAAGCACTGTAAGGATTGATTATGAAGTTAA	-2324

Fig 1 contd

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GATAAATCTCAGCAAGACATAAATGTGCAAGCACGGGATCCATGAATAAC -2274  
GAGCACTGACCATGTGGAAATGATAATCTTTGTTTCCTTTATTCCAGGCA -2224  
GTAAGGAGAAAGCGCTCACAGGGCTGCCTTACACCATTTTACTAGAGAGC -2174  
TAGCCTATGTCAGTCGGTAGCTGGCAATTACAAACTGAAGCAGTTCTAGT -2124  
TCATGTGGAGGATGAATTTAACCATAATCTCAACCCCTCTGCATGAAAC -2074  
AGAGACTAAGTACTCAAGTACCAGTTATCAGTCACTTACTATATGACAGG -2024  
CACTGTACTCAACAATTTACATGTATTATTGAATTACATGCCCCAACAC -1974  
TCTATGAGGAAGCTGAAGGTTAGAGAAGTATCTCATTTCATTATTACACAG -1924  
TGGCAAACCTGAGATCTGAACTCAGGTCTATCCAACCTCAGGACCTGAGAT -1874  
CCCAATTGCTACACAATTCTAATCAAGTTAAAAGGGAAAAAGGATTTGAT -1824  
TTGCTCAGAAGTGTATAGGGGCATATGTTACAATTATAACATTACAAAGA -1774  
TTTATATGTTGAAAAATAAATTTATCAAACAAATAAACTTTATAAGCCT -1724  
GATCTAATACTGCTCCGCAACAAAGACTATCTGAAATCCTTCAGGGCATC -1674  
TGGTTTGTGTCTGGTTTTCTTAATCTTTAATGATGGGCAAATCTAATGC -1624  
ATTATGTAAGGCCATTTTTTCTCAAGAGATGTAGATACCTCTTAAGAATT -1574  
TGATGAAAATGCATTAACCTTTTCAGGCTACTGAGTTGCATTTTAGTGCAC -1524  
TGAGGCAGTAAATTAGTGTACAATGTGCGAAAGTAGTGACCTAAAAAATA -1474  
AATATTTGATATGAACCACTGCACTCTCTTGGGGAAAAAAGTAATGGATT -1424  
AACTCTCTTAGGAGTCCTTAGCTTCCCCAAAAGTAGTAGGAAAAATAAAT -1374  
CTCCTGTGGCCTGGAAACAGCTTCTGTTTCTTGCTGGCTATATTTGTTTA -1324  
GGTTTTTAATAGTT**CATTTG**ATTAGACCTTGTGGCTCCCAAAGCTAAGGT -1274

E-box (4)

TGAGAGTTTGATCCCTACAGAGGCCACTTCAATTTAGAGAACAAAAAGCC -1224  
CCATTCTCTGCTCCCAGACCTTACCCCAAATCCCTGCCAGGTGTCTGCCC -1174  
TCCGGT**CAAATG**AGAACTGGCAAAGGAAGTACTAGGAGGTGCACAGTA -1124

E-box (3)

CTAGGAAGTAGAAAAATGGACTAGCACACTACTGAGAAGCAGAAAAATGG -1074

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GCACCCTTCATGATGGTGTTCCTTTCCCTTTCTGTGTTCACAATGCTCCG -1024  
 ATATAATTTACAGAGGGTAGATAACTACATTTTTTTCTTTTACCACTGGA -974  
 AGGCTGAGGAAACTTTGTTACCCATCATAAAATTCACATCTTCTAAGT -924  
 CATTCTATGTTATTCTAAGATCAAATAGCTGACAATATCCTCTTTGTAAT -874  
 AAACAATGAAAAACACATCCTCTGAGCAATATTAATCTGCAACTTTAGG -824  
 ATAGGAAGTAACTTAATACTAGTCAATTGAACTGAAATACAATTTTCAT -774  
 ATGAATAAAAGATATTATTTAAAGTAATTCCATGAGCAATTTAATATTA -724  
 AAGTAGGATTTTCATTATGTGTTAAGAATTTATTCAGGGAAACAAGTTTC -674  
 TCAAATTATAGCAGAAAATCTTTTACTAGTATCACAGTCTTTTCATTTAA -624  
 GTCTTCCTGAATAAATCTGTATTTTCTAATTATACAAGACTAAAAATAAT -574  
 MEF2-site  
 TTAATATAACAAATAAAATTATTTTTTACTTCAAATGCTTACTTAAATAGT -524  
 E-box (2)  
 ATAAATCATTTTATTTTCTGAGGGAAAAGCATATCAACTTTTTAAGTAT -474  
 TATA-box (3)  
 GAAGTGTAATTAAGATTTATTCACTTAAATTATAATTTTTTAAAGTTTCA -424  
 CATATAAAGATGAATAAGATCTAAGTGTATATGTTATTGTTAATAAAGTT -374  
 TTTAATTTTTCGCATGTCACATACAGCCTTTATTATTCATAGATTTATTC -324  
 CTTTTAAGAAGTAGTCAAATGAATCAGCTCACCTTGACTGTAACAAAAT -274  
 E-box (1)  
 ACTGTTTGGTGACTTGTGACAGACAGGGTTTTAACCTCTGACAGCGAGAT -224  
 TCATTGTGGAGCAAGAGCCAATCACAGATCCCGACGACACTTGTCTCATC -174  
 CAAT-box  
 AAAGTTGGAATATAAAAAGCCACTTGGAATACAGTATAAAAAGATTCACTG -124  
 TATA-box (2) TATA-box (1)  
 GTGTGGCAAGTTGTCTCTCAGACTGGGCAGGCATTAACGTTTGGCTTGGC -74  
 GTTACTCAAAAGCAAAAGAAAAGTAAAAGGAAGAAGTAAGAACAAGGGAA -24

Fig 1 contd



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AAGATTGTATTGATTTTAAACCATGCAAAACTGCAAATCTCTGTTTAT +27  
 ATTTACCTATTTATGCTGATTGTTGCTGGCCCAGTGGATCTGAATGAGAA +77  
CAGCGAGCAGAAG +90

FIG. 1. Nucleotide sequence of the 10,492-basepair promoter-enhancer region of bovine myostatin. Total length of the DNA sequence is 10,492 basepairs (bps) which consist of 10,402 bps of upstream and 90 bps of coding sequence. The coding sequence of myostatin is underlined. Nucleotides and the relative position of putative nucleotide motifs are numbered with respect to the translation start site (+1 bp). Consensus sequences for basic functional elements of a mammalian promoter (TATA and CAAT boxes) and for known muscle specific transcription factors (E-box and MEF2 sites) are bolded in the sequence and they are listed below.

TATA-boxes[1]: -139 bps(1); -163 bps(2);  
 -524 bps(3)  
 CAAT-box[2]: -206 bps  
 E-boxes[3]: -308 bps(1); -543 bps(2)  
 -1167 bps(3); -1309 bps(4)  
 MEF2 site[4]: -584 bps

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## Myostatin Promoter Activity

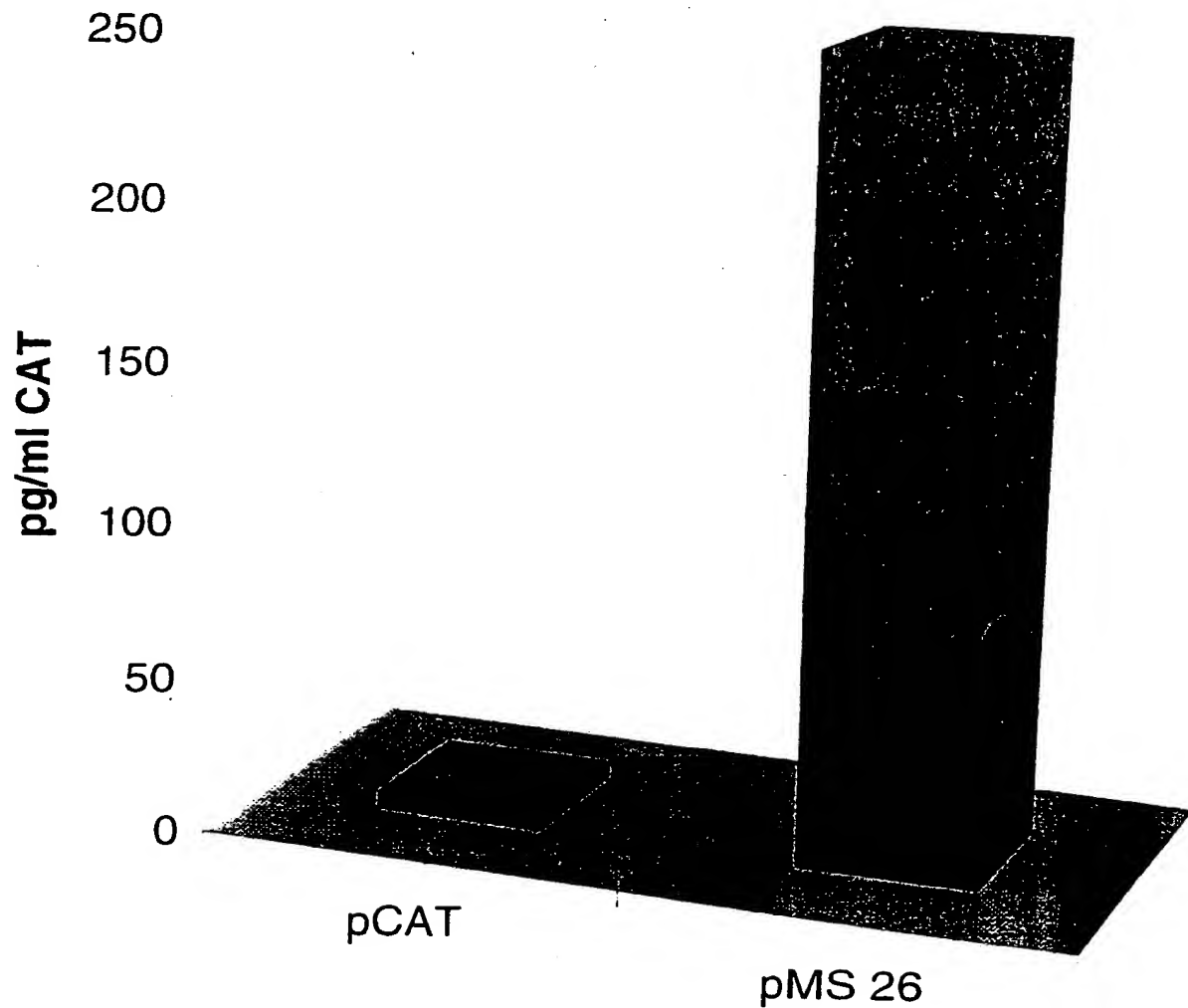


Fig 2